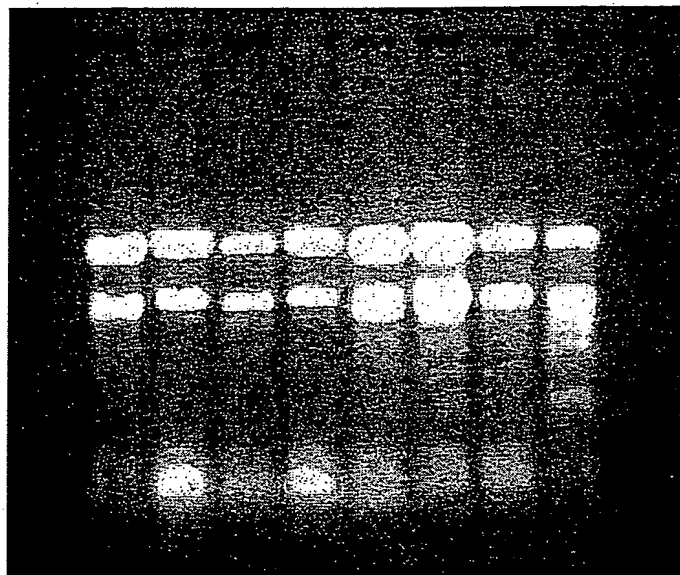


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1 2 3 4 5 6 7 8

A



1 2 3 4 5 6 7 8

B

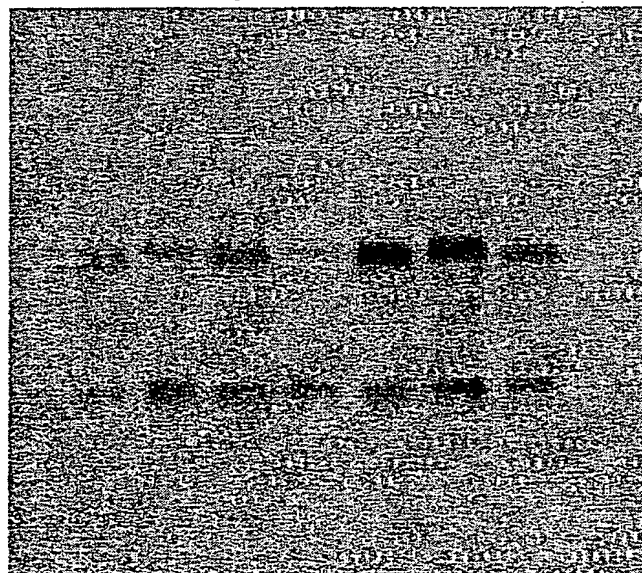


Fig.1

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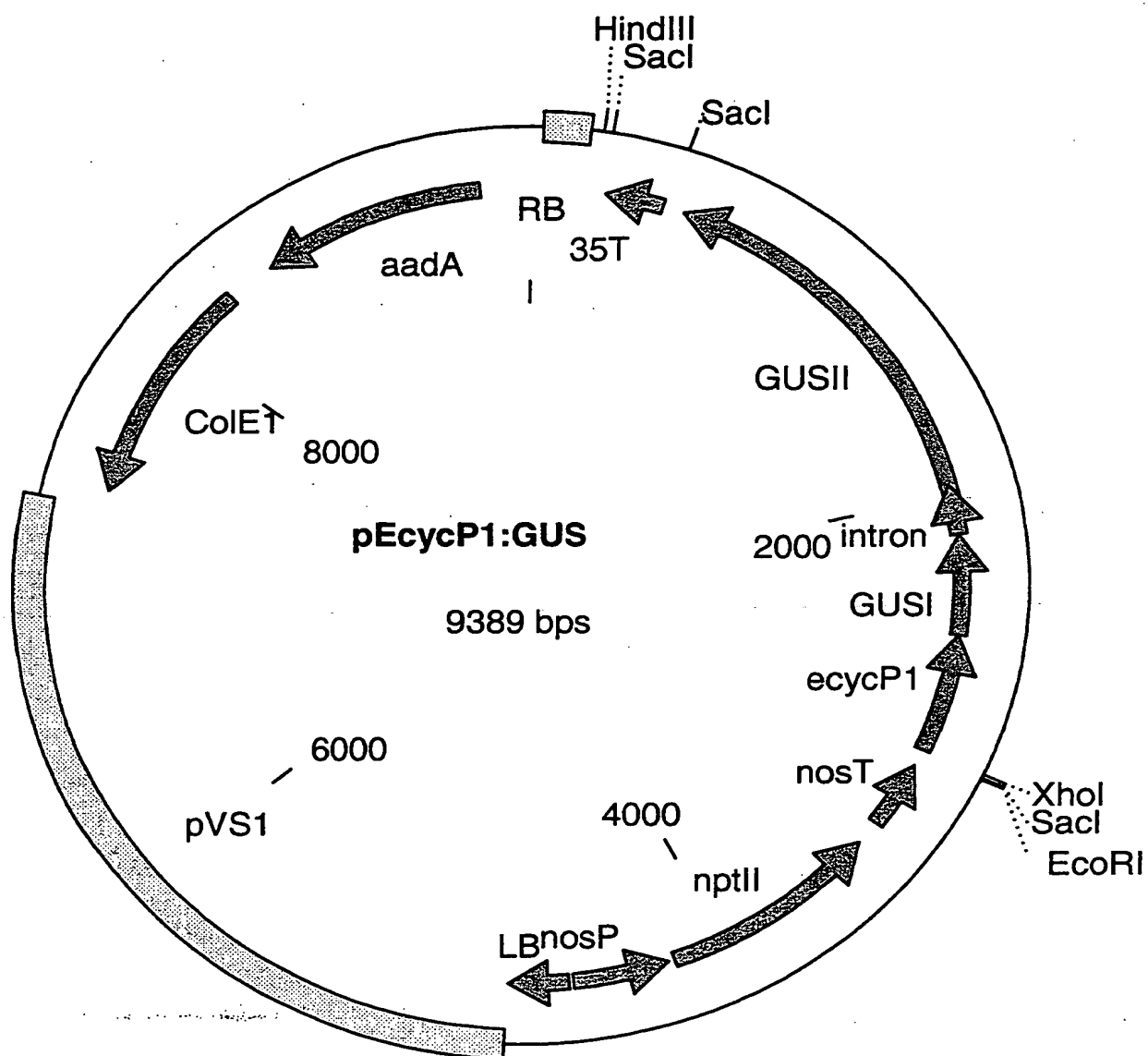


Fig.2

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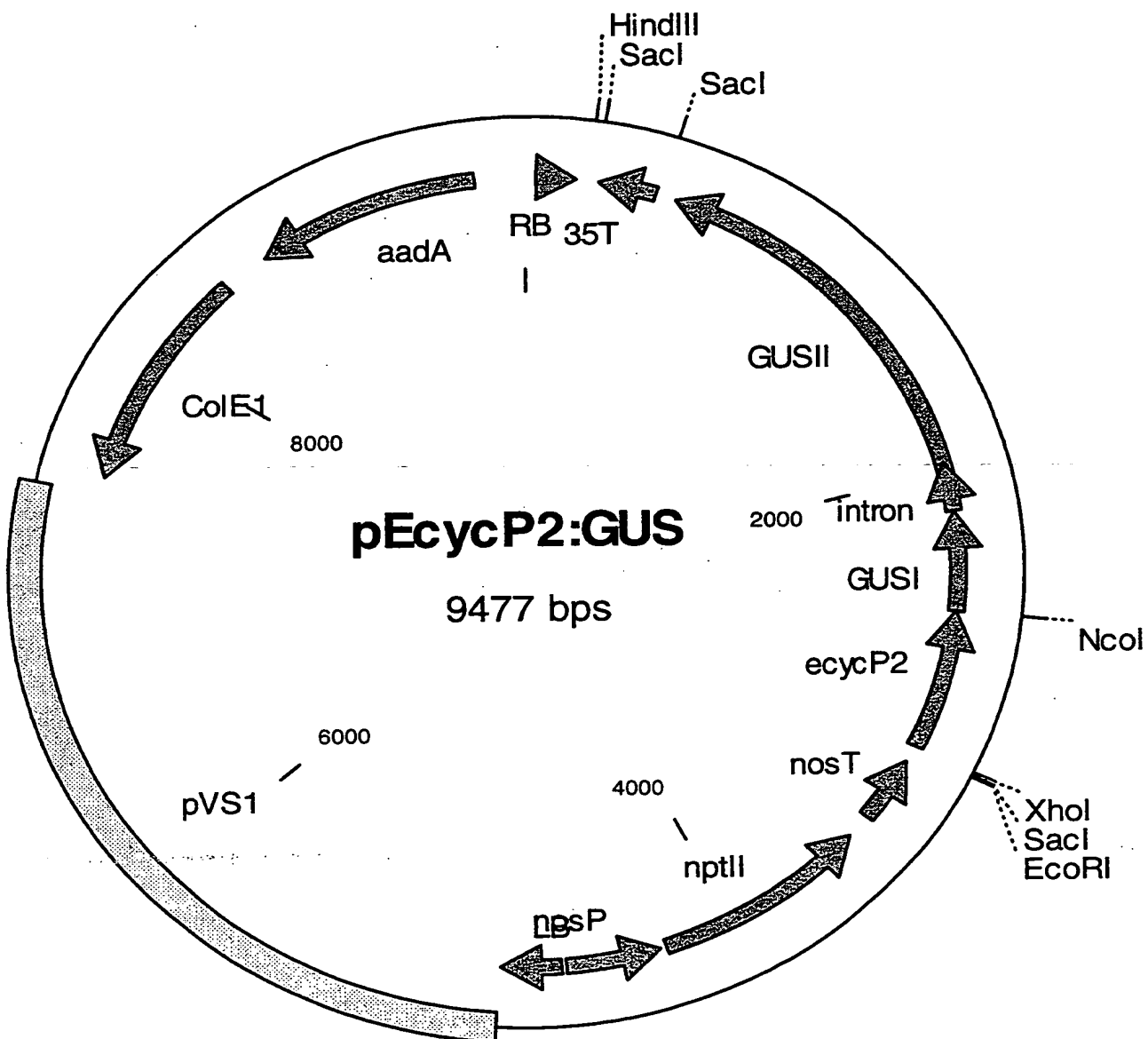


Fig.3

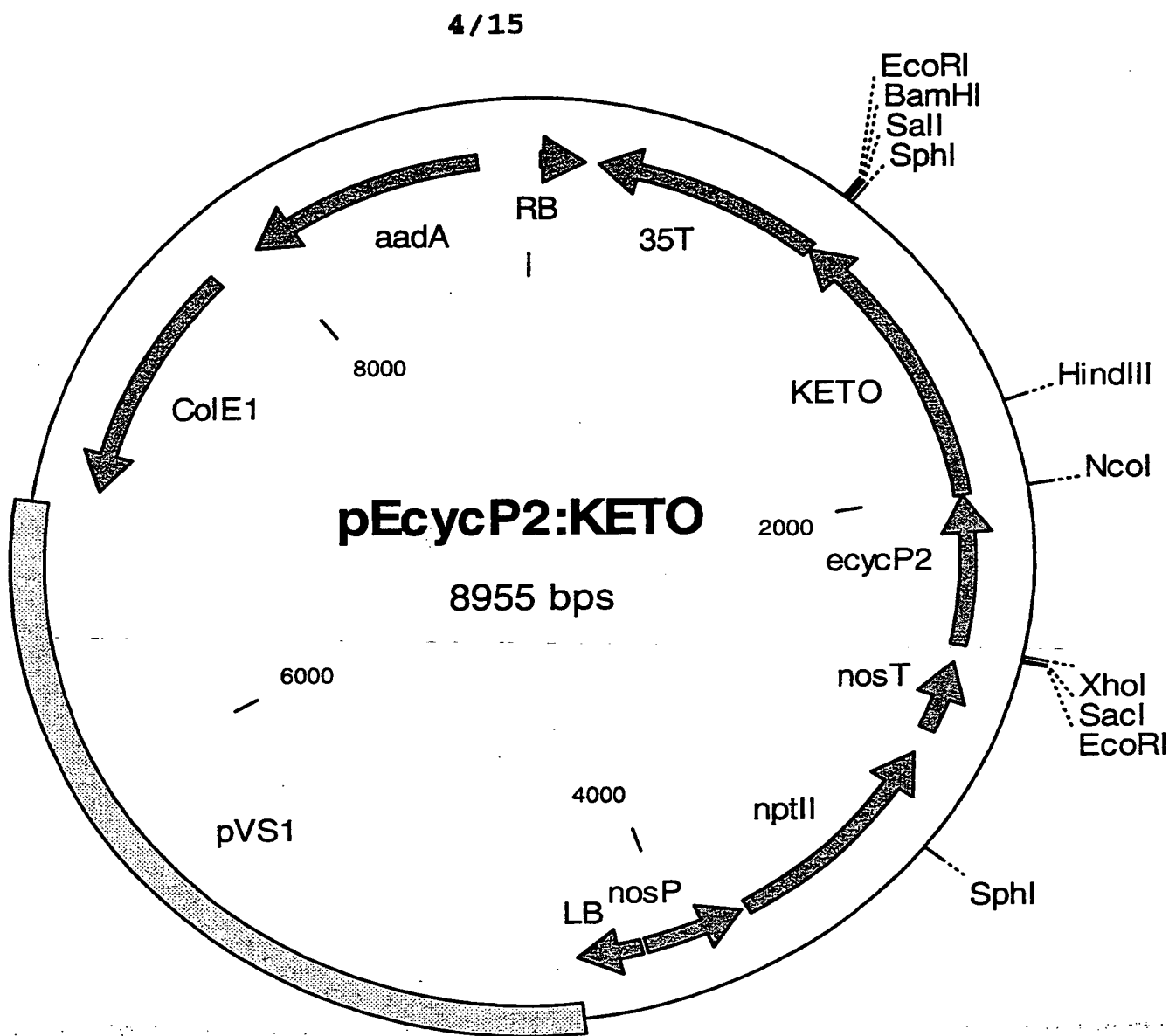


Fig.4

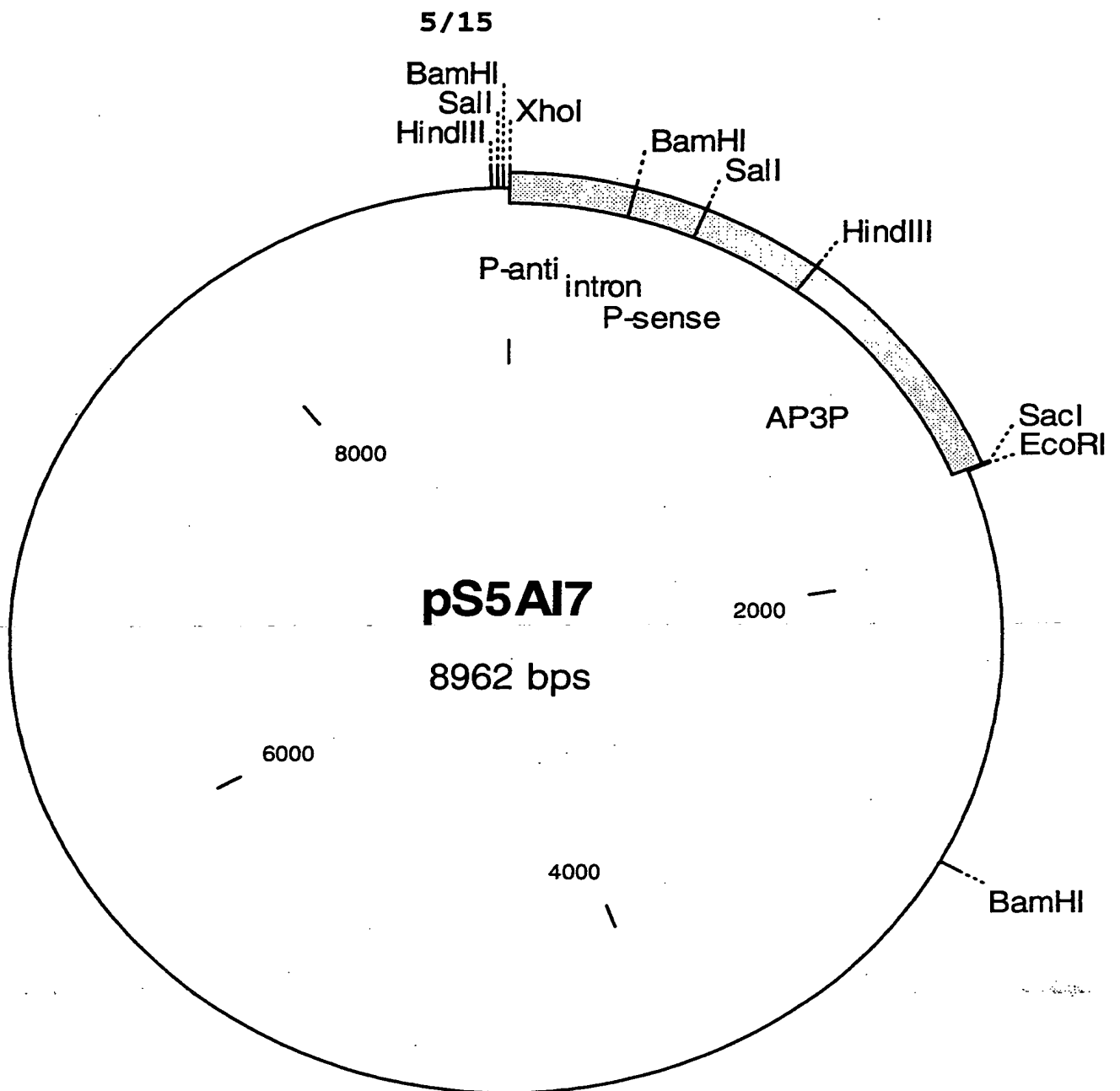


Fig.5

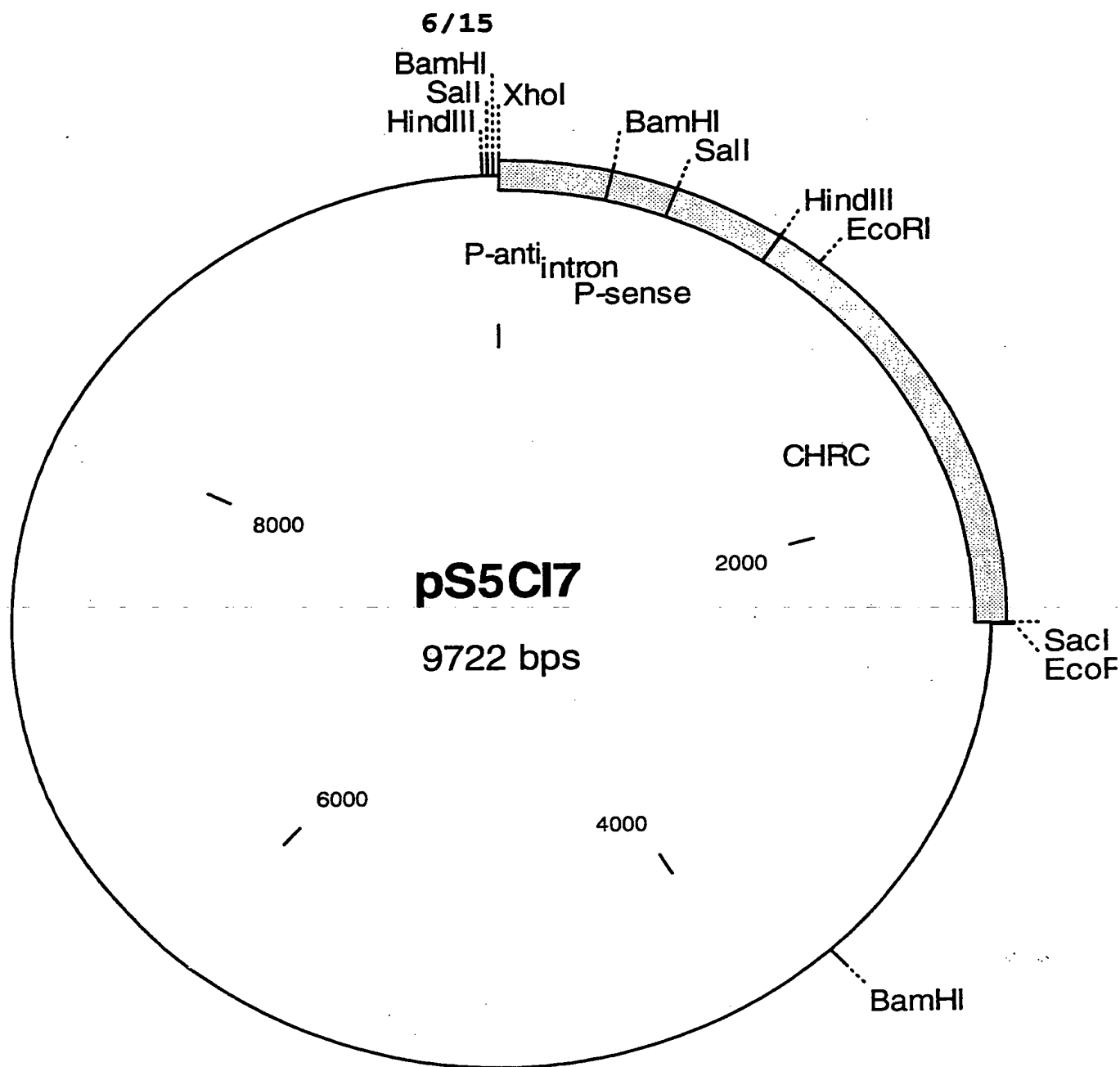


Fig.6

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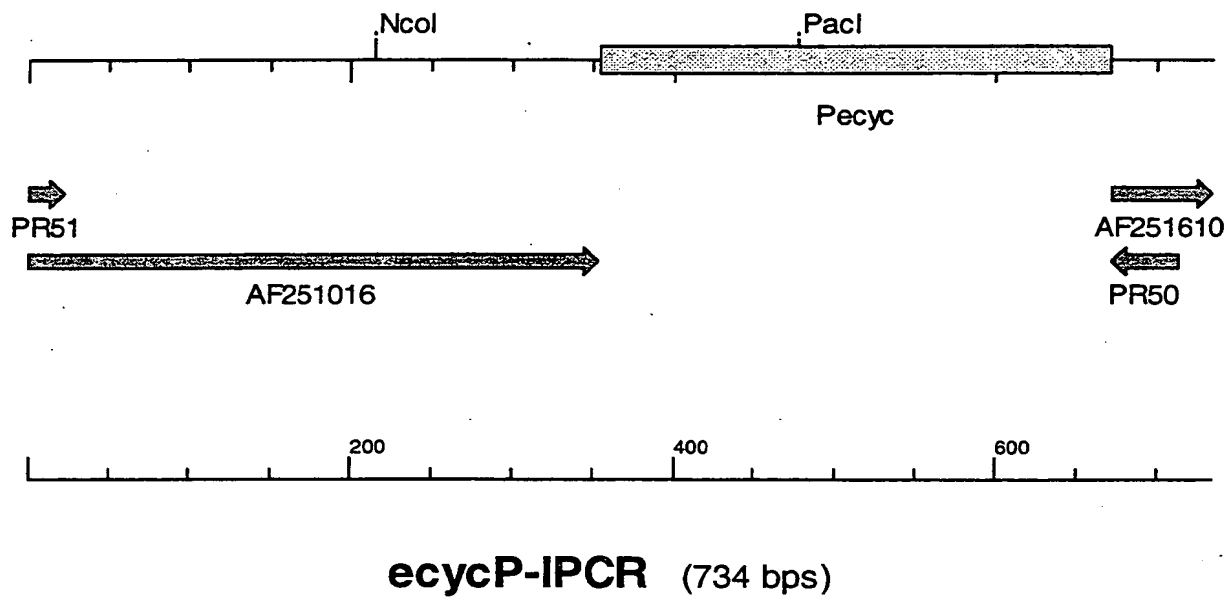


Fig.7

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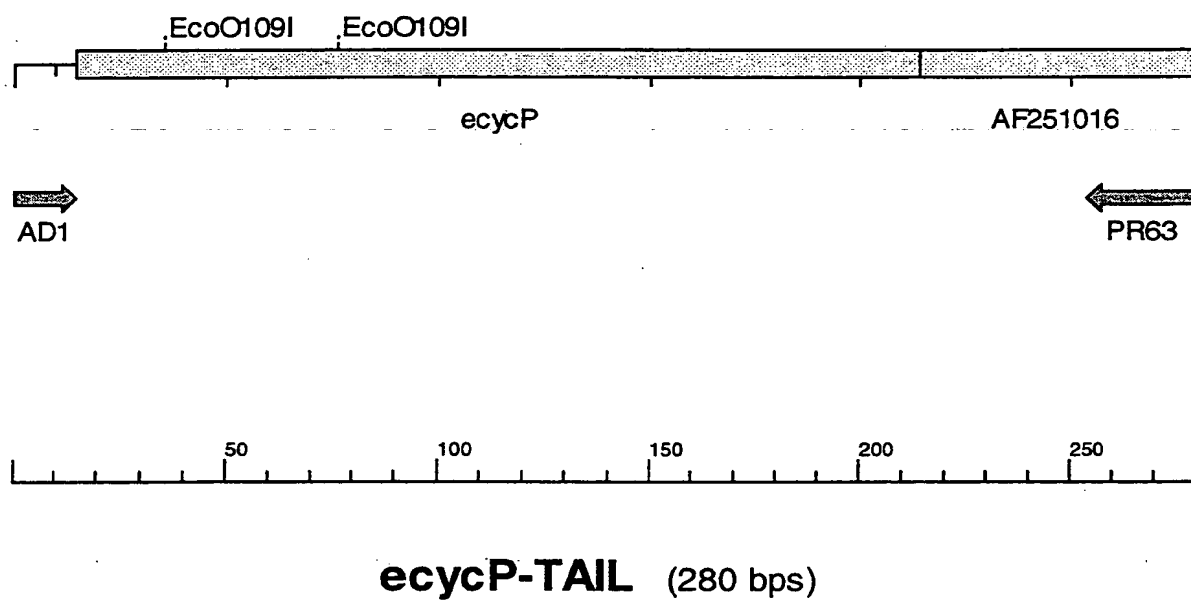


Fig.8



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**Fig. 9**

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|            |   |     |
|------------|---|-----|
| KETO2.pro  | MQLAATVMLEQLTGSAEALKEKEKEVAGSSDVLRTWATQYSLPSEESDAA      | 50  |
| X86782.pro | MQLAATVMLEQLTGSAEALKEKEKEVAGSSDVLRTWATQYSLPSEESDAA      | 50  |
| KETO2.pro  | RPGLKNAYKPPPSDTKGI TMALAVI GSWAAVFLHAI FQI KLPTSLDQLHW  | 100 |
| X86782.pro | RPGLKNAYKPPPSDTKGI TMALRVI GSWAAVFLHAI FQI KLPTSLDQLHW  | 100 |
| KETO2.pro  | LPVSDAT AQLVSGSSSLLHI VVVVFFVLEFLYTGLFI TTHDAMHGTI AMRN | 150 |
| X86782.pro | LPVSDAT AQLVSGTSSLLDI VVVVFFVLEFLYTGLFI TTHDAMHGTI AMRN | 150 |
| KETO2.pro  | RQLNDFLGRVCI SLYAWFDYNNMLHRKHWEHHNHTGEVGKDPDFHRGNPGI    | 200 |
| X86782.pro | RQLNDFLGRVCI SLYAWFDYNNMLHRKHWEHHNHTGEVGKDPDFHRGNPGI    | 200 |
| KETO2.pro  | VPWFASFMSYMSMWQFARLAWWT VVMQLLGAPMANLLVFMAAAPILSAF      | 250 |
| X86782.pro | VPWFASFMSYMSMWQFARLAWWT VVMQLLGAPMANLLVFMAAAPILSAF      | 250 |
| KETO2.pro  | RLFYFGTYMPHKPEPGAA SSSPA VMNWWKSRTSQA SSDLVSFLT CYHFDL  | 300 |
| X86782.pro | RLFYFGTYMPHKPEPGAA SSSPA VMNWWKSRTSQA SSDLVSFLT CYHFDL  | 300 |
| KETO2.pro  | HWEHHRWPFA PWWE L PNCRRRL SGRGL VPA                     | 329 |
| X86782.pro | HWEHHRWPFA PWWE L PNCRRRL SGRGL VPA                     | 329 |

Fig.10

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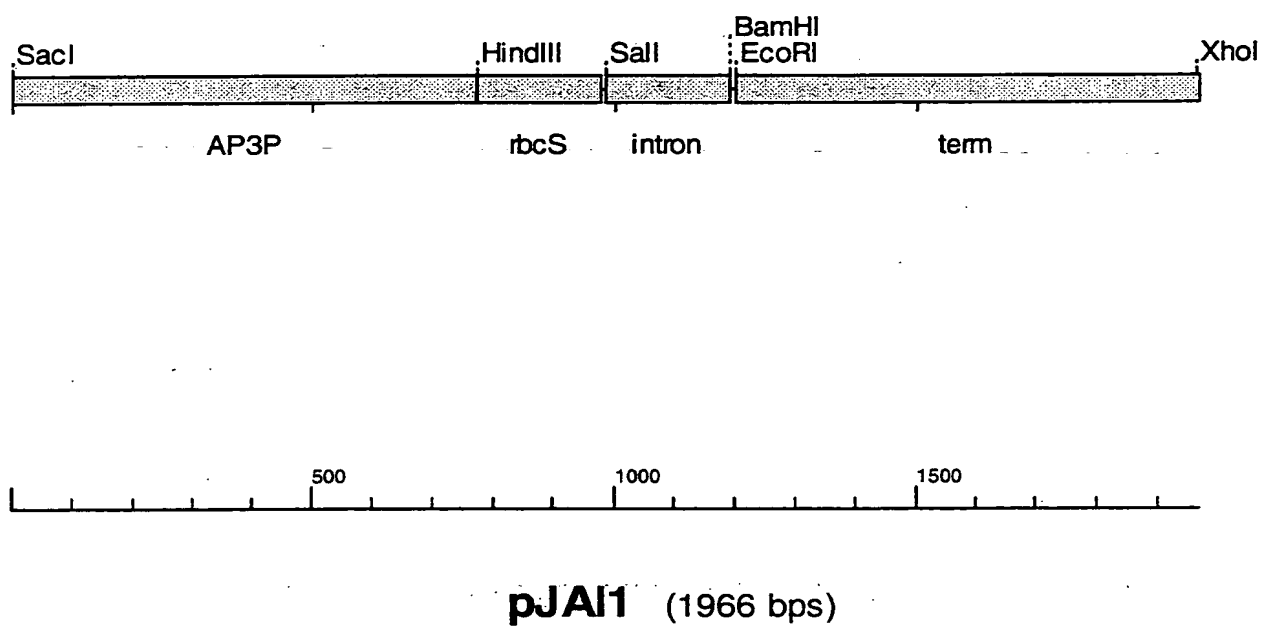


Fig.11

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|           | 1   | 10   | 20      | 30   | 40                                  | 50  | 60  | 70  | 80  | 90  | 100 |
|-----------|-----|--|---------|--|-------------------------------------|-----|-----|-----|-----|-----|-----|
| A         | (1) | MLPFLSSLLNGVTDNPCRKAMDITLLKTHINKLEFLPQVHGALEKS | ---     | SSLSLKIQIQNELRFGLKKSRQNRNSCFIKASSSALLELPEVETKK | ---                                 |     |     |     |     |     |     |
| B         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| C         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| D         | (1) | ---  | MSMRAG  | ---  | HMTATMAAFTCPFRMTS                   | --- | --- | --- | --- | --- | --- |
| E         | (1) | ---  | MELLGVR | ---  | NLISSCPVMIFGIRNLSSSKLAVNIHRYG       | --- | --- | --- | --- | --- | --- |
| F         | (1) | ---  | MELLGVR | ---  | NLISSCPVMIFGIRNLSSSKLAVNIHRYG       | --- | --- | --- | --- | --- | --- |
| G         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| H         | (1) | ---  | MECTGAR | ---  | NMTATMAVFTCPFRFTDCNIRHKFSLLKQRRFTNL | --- | --- | --- | --- | --- | --- |
| I         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| J         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| K         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| L         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| M         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| N         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| O         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| P         | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |
| Consensus | (1) | ---  | ---     | ---  | ---                                 | --- | --- | --- | --- | --- | --- |

|           | 101   | 110   | 120 | 130 | 140 | 150 | 160 | 170 | 180 | 190 | 200 |
|-----------|-------|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| A         | (101) | ---   | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| B         | (91)  | ---   | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| C         | (1)   | ---   | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| D         | (69)  | SMDAQSSLSQKLPVPIGGGDSNCILDLVWIGGPAGLALAGESAKLGINVALIG | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| E         | (87)  | SMEKQAKLADKLPPIPG                                     | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| F         | (87)  | SMEKQAKLADKLPPIPG                                     | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| G         | (1)   | ---   | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| H         | (92)  | SMESQSKLSEKLAQIPIG                                    | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| I         | (1)   | ---   | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| J         | (75)  | AMDCYSKLSDKLRQISDA                                    | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| K         | (1)   | ---   | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| L         | (97)  | SMDSQSKLSSKLLPDPEN                                    | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| M         | (69)  | SMDAQSSLSQKLPVPIGGGDSNCILDLVWIGGPAGLALAGESAKLGINVALIG | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| N         | (66)  | ---   | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| O         | (88)  | DMDEQSKLVKLPPISIG                                     | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| P         | (85)  | DMDOQSKLSDLELRQISAG                                   | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Consensus | (101) | MD QS LS KLP I G                                      | --- | --- | --- | --- | --- | --- | --- | --- | --- |

Fig.12A

(201) 201 210 220 230 240 250 260 270 280 290 300  
 A DLNRPYGRVNRKLLKSKMLQKCTINGVKFHQAKVTKVTHEE--SKSLICNDGVITQAAVLDATGFSRCLVQVDKPNP--GYQVAYGILAEVBOHPFDL  
 B MIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYEVGGPRVSVQIAYGVEVEVNNPYDP  
 C (1) -IGRAYGLVAICFMKNCLKGVSSQVFRILAQKLKRLKLEWATAMLVKITILSFHAGILILHLEQLGNPCSMGLGVPEFLSKQIMVSRIRWKPPIPYDP  
 D LIGRAYGRVSRDILLHEELLJRCMESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 E LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 F LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 G LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 H LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 I LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 J YIGRSYGVSRQILLHEELLVHRCLESVSYLNKVENINMEGPDGHRVACIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 K LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 L MIGRAYGRVSRDILLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 M LIGRAYGRVSRDILLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 N DLSRPYGRVNRKQKSKMLQKCTINGVKFHQAKVTKVTHEE--ANSTVCSGDKVQIQAASVLDATGFSRCLVQVDKPNP--GYQVAYGILAEVBOHPFDL  
 O TIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 P LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLVECENNIVIPCLATVASGAASEKLLQYELGGPRVCVQIAYGVEVEVNNPYDP  
 Consensus (201) LIGRAYGRVSR LLHEELLKRCVESGVSYLSKVEKLIIEAGDCHSLV CE I IPCLATVASGAASEKLL YEVGGPRVCVQIAYGVEVEVNNPYDP

(301) 301 310 320 330 340 350 360 370 380 390 400  
 A DKMVFMDWRDSDHANNNSQLKEANSKIPITFLYAMPPSSNRIFLEETSIVARPGVPMKDIQERWVARLKHGLGKVKSEED-----EHCVIIPMGGLP  
 B SLIMVFMDYRDYTKQKVPQME---AEYPTFLYAMP-----  
 C SLIMVFMDYRDYTKQKVPQME---AEYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 D SLIMVFMDYRDYTKHKSQSLE---AQYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 E SLIMVFMDYRDYTKHKSQSLE---EEYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 F SLIMVFMDYRDYTKHKSQSLE---EEYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 G SLIMVFMDYRDYTKHKSQSLE---AKYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 H SLIMVFMDYRDYTKHKSQSLE---AKYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 I SLIMVFMDYRDYTKHKSQSLE---AKYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 J SLIMVFMDYRDYTKHKSQSLE---AKYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 K SLIMVFMDYRDYTKHKSQSLE---QGNPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 L SLIMVFMDYRDYTKHKSQSLE---AQYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 M SLIMVFMDYRDYTKHKSQSLE---AQYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 N DKMVFMDWRDSDHANNNSQLKEANSKIPITFLYAMPPSSNRIFLEETSIVARPGVPMKDIQERWVARLKHGLGKVKSEED-----EHCVIIPMGGLP  
 O DQWVFMDYRDYTKHKSQSLE---AEYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 P SLIMVFMDYRDYTKHKSQSLE---AKYPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EMSYIIPVGGSLP  
 Consensus (301) SLIMVFMDYRDYTK KV SLE A YPTFLYAMMSPRIFFEEHICLASKDAMPFDLLKKKIMSRLL QIMGIRVAKIYEE EMSYIIPVGGSLP

Fig.12B

(401) 401 410 420 430 440 450 460 470 480 490 500  
 A VLFQRVWGIGGTAGMHPSTGYMVARITLAAPIVANAIVRSLS--D-----RSISGKLSAEVWKDLWPIERRRQREFFCFQMDILLKLDLPATRFFF  
 B (166) -----  
 C (188) NTEQKNLAFGAAAR-----  
 D (355) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPNVAATIAKILGKNSKQMLDHCRYTTN-ISKQAMETLWPLERKRQRAFFLFGELALIVQMDIEGIRFFF  
 E (368) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPKVASVIAKILKQNSAYVVSQSSAVN-ISMQAMSSILWPKERKRQRAFFLFGELALIVQMDIEATRFFF  
 F (368) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPKVASVIAKILKQNSAYVVSQSSAVN-ISMQAMSSILWPKERKRQRAFFLFGELALIVQMDIEATRFFF  
 G (222) NTEQKITLAFGAAASWHPATGYSVRSLSSEAPKCAFVLNLRQNHSHKMLTSS-SIPS-ISTQAMNITLWPKERKRQSSFFLFGELALILQDIEGIRFFF  
 H (373) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPNVAATIAKILRQDQSKEMISLGKVTN--ISKQAMETLWPLERKRQRAFFLFGELSHIVLMDIEGIRFFF  
 I (249) NTEQKNLAYGAAAS-----  
 J (356) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPKVASAIAANLKNLISKNAILLRQSVGN-ISMQAMNITLWPKERKRQRAFFLFGELSLIVQDIEGIRFFF  
 K (276) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPNVAATIAVILKDHSHRGLTHQSNEN-ISMQAMNITLWPKERKRQRAFFLFGELALILQDIEGIRFFF  
 L (378) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPRYASVTSIDILNRVYFGEVILPGTSQSSPSMLAWRTLWPKERKRQSSFFLFGELALILQDIEGIRFFF  
 M (364) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPNVAATIAKILGKNSKQMLDLGRYTTN-ISKQAMETLWPLERKRQRAFFLFGELALIVQMDIEGIRFFF  
 N (345) VLFQRVWGIGGTAGMHPSTGYMVARITLAAPIVANAIVRVLGSP-SS-----NSLRGQDLSAEVWRDLWPIERRRQREFFCFQMDILLKLDLDAATTRFFF  
 O (369) NTEQKNLAFGAAASWHPATGYSVRSLSSEAPKVASVIAELLREETT-----KQINSN-ISRQAMDTLWPKERKRQRAFFLFGELALIVQDIEGIRFFF  
 P (366) NTEQKITLAFGAAASWHPATGYSVRSLSSEAPKCAVLANILRQHYSHKMLTSS-SIPS-ISTQAMNITLWPKERKRQSSFFLFGELALILQDIEGIRFFF  
 Consensus (401) NTEQKNLAFGAAASWHPATGYSVRSLSSEAP YASVIA ILR S L IS QAW TLMP ERKRQRAFFLFGELALIVQDIEG RFFF

(501) 501 510 520 530 540 550 563  
 A DAFFDLERYMHGFLSSRLFTPELLVFGLSLFSHASNTSRLEIMAKGTILPLVAMNINLVQDID  
 B (166) -----  
 C (202) -----  
 D (454) RTFFRLPTWMMGFLGSSLSSTDLILFAFYMFIIAPHSLRMGLVRHLLSDPTGGIMLKAYLITI  
 E (467) RTFFRLPTWMMGFLGSSLSSTDLVLFSMYMFVLAENSMRMSLVRHLLSDPSGAVMWKAYLER  
 F (467) RTFFRLPTWMMGFLGSSLSSTDLVLFSMYMFVLAENSMRMSLVRHLLSDPSGAVMWKAYLER  
 G (320) RAFFRVPKMMQGFGLGSSLSXADIMLFAFYMFIIAPNDMRRGLIRHLLSDPTGATLIRTYLITF  
 H (471) RTFFRLPKMMMGFLGSSLSSTDLILFALYMFVIAPHSLRMELVRHLLSDPTGATMWKAYLITI  
 I (263) -----  
 J (455) RTFFRVPKMMMGFLGSSLSSTDLILFAFYMFIIAPNDLPMGLIRHLLSDPTGATMIRTYITIL  
 K (375) RTFFRLPKMMMHGFLGSSLSSTADLILFAFYMFIIAPNDLRKCLIRHLVSDPTGATMWRTYITIL  
 L (478) ETFFRLPKMMRGFLGSTLSSVDLILFAFYMFIIAPNQMRMNLVRHLLSDPTGSTIMIKTYLITL  
 M (463) RTFFRLPTWMMMGFLGSSLSSTDLILFAFYMFIIAPHSLRMGLVRHLLSDPTGGIMLKAYLITI  
 N (439) DAFFDLQPHYMHGFLSSRLFTPELLVFGLSLFSHASNTSRLEIMPKGIVPLAKMINNLVQDRD  
 O (462) RTFFRLPKMMQGFGLGSLTITSGDLVLFALYMFVISPNNLRKGLINHLISDPTGATMIKTYILKV  
 P (464) RAFFRVPKMMQGFGLGSSLSSTADIMLFAFYMFIIAPNDMRRGLIRHLLSDPTGATLIRTYLITF  
 Consensus (501) RTFFRLP WMM GFLGSSLS DLILFA YMFIIAPN ILM LVRHLLSDPTGATMIK YLIT

Fig.12C

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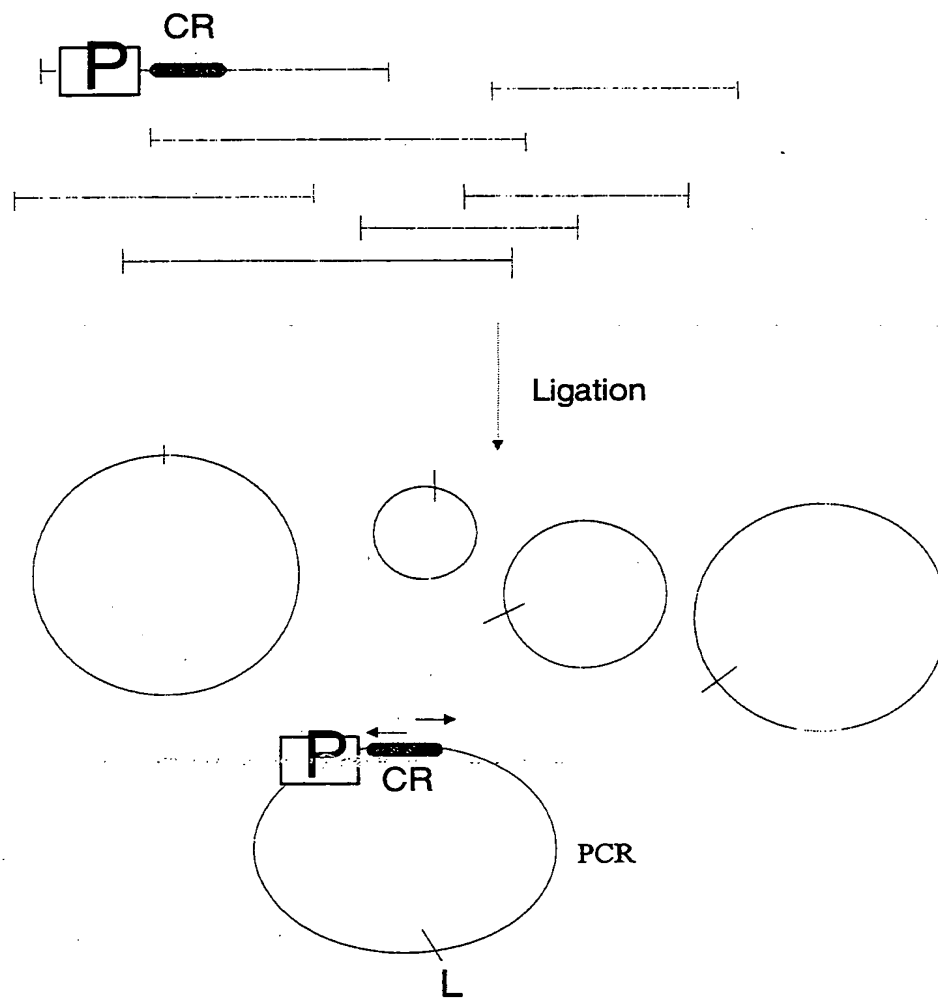


Fig. 13

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